



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 / 734,583A
Source: TEWK
Date Processed by STIC: 11/5/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. ~~Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):~~
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

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Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/234,583A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u> ✓ </u> Variable Length	Sequence(s) <u> 8 </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/734,583A

DATE: 11/05/2004
 TIME: 14:52:42

Input Set : A:\87534-3000.txt
 Output Set: N:\CRF4\11052004\I734583A.raw

3 <110> APPLICANT: Hornik, Vered
 5 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN
 ANALOGS
 7 <130> FILE REFERENCE: 87534-3000
 9 <140> CURRENT APPLICATION NUMBER: 09/734,583A
 10 <141> CURRENT FILING DATE: 2000-12-13
 12 <160> NUMBER OF SEQ ID NOS: 10
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 14
 18 <212> TYPE: PRT
 19 <213> ORGANISM: mammalian
 21 <400> SEQUENCE: 1
 23 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
 24 1 5 10
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 6
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <221> NAME/KEY: DISULFIDE BRIDGE
 34 <222> LOCATION: (1)..(1)
 35 <223> OTHER INFORMATION: Cys residues at amino acid positions and 6 form a disulfide
 bridge
 39 <220> FEATURE:
 40 <221> NAME/KEY: MOD_RES
 41 <222> LOCATION: (3)..(3)
 42 <223> OTHER INFORMATION: The Trp residue is the D isomer
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: Synthetic peptide
 49 <400> SEQUENCE: 2
 51 Cys Phe Trp Lys Thr Cys
 52 1 5
 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 6
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <221> NAME/KEY: MOD_RES
 62 <222> LOCATION: (1)..(1)
 63 <223> OTHER INFORMATION: N-Methyl
 66 <220> FEATURE:
 67 <221> NAME/KEY: MOD_RES
 68 <222> LOCATION: (1)..(6)

Does Not Comply
 Corrected Diskette Needed

pp 1,618

insert
 "1"

69 <223> OTHER INFORMATION: cyclo

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/734,583A

DATE: 11/05/2004
 TIME: 14:52:42

Input Set : A:\87534-3000.txt
 Output Set: N:\CRF4\11052004\I734583A.raw

72 <220> FEATURE:
 73 <221> NAME/KEY: MOD_RES
 74 <222> LOCATION: (3)..(3)
 75 <223> OTHER INFORMATION: The Trp residue is the D isomer
 77 <220> FEATURE:
 78 <223> OTHER INFORMATION: Synthetic peptide
 81 <400> SEQUENCE: 3
 83 Ala Tyr Trp Lys Val Phe
 84 1 5
 87 <210> SEQ ID NO: 4
 88 <211> LENGTH: 8
 89 <212> TYPE: PRT
 90 <213> ORGANISM: Artificial Sequence
 92 <220> FEATURE:
 93 <221> NAME/KEY: MOD_RES
 94 <222> LOCATION: (1)..(1)
 95 <223> OTHER INFORMATION: The Phe residue is a D isomer
 98 <220> FEATURE:
 99 <221> NAME/KEY: MOD_RES
 100 <222> LOCATION: (8)..(8)
 101 <223> OTHER INFORMATION: The Thr residue ends with CH2OH
 104 <220> FEATURE:
 105 <221> NAME/KEY: DISULFIDE BRIDGE
 106 <222> LOCATION: (2)..(2)
 107 <223> OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
 110 <220> FEATURE:
 111 <221> NAME/KEY: MOD_RES
 112 <222> LOCATION: (4)..(4)
 113 <223> OTHER INFORMATION: The Trp residue is a D isomer
 116 <220> FEATURE:
 117 <223> OTHER INFORMATION: Synthetic peptide
 120 <400> SEQUENCE: 4
 122 Phe Cys Phe Trp Lys Thr Cys Thr
 123 1 5
 126 <210> SEQ ID NO: 5
 127 <211> LENGTH: 7
 128 <212> TYPE: PRT
 129 <213> ORGANISM: Artificial Sequence
 131 <220> FEATURE:
 132 <221> NAME/KEY: DISULFIDE
 133 <222> LOCATION: (2)..(2)
 134 <223> OTHER INFORMATION: A Disulfide Bridge is formed between the Cys residues at
 position
 135 2 and 6
 137 <220> FEATURE:
 138 <221> NAME/KEY: MOD_RES
 139 <222> LOCATION: (1)..(1)
 140 <223> OTHER INFORMATION: The Phe residue is a D isomer
 143 <220> FEATURE:
 144 <221> NAME/KEY: MOD_RES

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/734,583A

DATE: 11/05/2004
 TIME: 14:52:42

Input Set : A:\87534-3000.txt
 Output Set: N:\CRF4\11052004\I734583A.raw

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145 <222> LOCATION: (4)..(4)
146 <223> OTHER INFORMATION: The Trp residue is a D isomer
149 <220> FEATURE:
150 <221> NAME/KEY: MOD_RES
151 <222> LOCATION: (7)..(7)
152 <223> OTHER INFORMATION: The Thr residue ends with N2H
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Synthetic peptide
159 <400> SEQUENCE: 5
161 Phe Cys Phe Trp Lys Cys Thr
162 1 5
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 8
167 <212> TYPE: PRT
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <221> NAME/KEY: MISC_FEATURE
172 <222> LOCATION: (1)..(1)
173 <223> OTHER INFORMATION: is a gamma amino butyric acid, diamino butyric acid, Gly,
beta-Al
174 a, 5-amino pentanoic acid or amino hexanoic acid; Residue 1 is bridged
175 to Residue 8; Residue 1 also begins with a hydrogen, or a m
176 ono- or di- saccharide attached
179 <220> FEATURE:
180 <221> NAME/KEY: MISC_FEATURE
181 <222> LOCATION: (2)..(2)
182 <223> OTHER INFORMATION: is (D) or (L) Phe or Tyr
185 <220> FEATURE:
186 <221> NAME/KEY: MISC_FEATURE
187 <222> LOCATION: (3)..(3)
188 <223> OTHER INFORMATION: is (D) or (L)-Trp, or (L)-Phe, (D)- or (L)-1Nal or (D) or
(L)-2Na
189 l, or Tyr
192 <220> FEATURE:
193 <221> NAME/KEY: MISC_FEATURE
194 <222> LOCATION: (4)..(4)
195 <223> OTHER INFORMATION: is (D) or (L)-Trp
198 <220> FEATURE:
199 <221> NAME/KEY: MISC_FEATURE
200 <222> LOCATION: (5)..(5)
201 <223> OTHER INFORMATION: is (D) or (L)-Lys
204 <220> FEATURE:
205 <221> NAME/KEY: MISC_FEATURE
206 <222> LOCATION: (6)..(6)
207 <223> OTHER INFORMATION: is Thr, Gly, Abu, Ser, Cys, Val, (D) or (L)-Ala, or (D)- or
(L)-A
208 la, or Tyr
211 <220> FEATURE:
212 <221> NAME/KEY: MISC_FEATURE
213 <222> LOCATION: (7)..(7)
214 <223> OTHER INFORMATION: is (D) or (L)-Phe, or (D)- or (L)-Ala, Nle, or Cys;
217 <220> FEATURE:

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RAW SEQUENCE LISTING
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Input Set : A:\87534-3000.txt
Output Set: N:\CRF4\11052004\I734583A.raw

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218 <221> NAME/KEY: MISC_FEATURE
219 <222> LOCATION: (8)..(8)
220 <223> OTHER INFORMATION: is Gly, Val, Leu, (D) or (L)-Phe, or 1Nal or 2Nal; with a
termina
221      1 carboxy acid, amide or alcohol group.
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Synthetic peptide
228 <400> SEQUENCE: 6
W--> 230 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
231      1      5
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 7
236 <212> TYPE: PRT
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <221> NAME/KEY: MISC_FEATURE
241 <222> LOCATION: (1)..(1)
242 <223> OTHER INFORMATION: is (D)- or (L)-Phe, or (D)- or (L)-Ala; wherein Residue 1 is
brid
243      ged to Residue 6 a bridging group composed of 1 to 5 methyl space
244      rs connected to an amide, thioether, thioester, or disulfide, fol
245      lowed by 1 to 5 methyl spacers
248 <220> FEATURE:
249 <221> NAME/KEY: MISC_FEATURE
250 <222> LOCATION: (2)..(2)
251 <223> OTHER INFORMATION: is Tyr or (D)- or (L)-Phe
254 <220> FEATURE:
255 <221> NAME/KEY: MISC_FEATURE
256 <222> LOCATION: (3)..(3)
257 <223> OTHER INFORMATION: is (D)- or (L)-Trp, (D)- or (L)-1Nal, or (D)- or (L)-2Nal
260 <220> FEATURE:
261 <221> NAME/KEY: MISC_FEATURE
262 <222> LOCATION: (5)..(5)
263 <223> OTHER INFORMATION: is Thr, Val, Ser, or Cys
266 <220> FEATURE:
267 <221> NAME/KEY: MISC_FEATURE
268 <222> LOCATION: (6)..(6)
269 <223> OTHER INFORMATION: is Gly or (D)- or (L)-Phe
272 <220> FEATURE:
273 <221> NAME/KEY: MISC_FEATURE
274 <222> LOCATION: (7)..(7)
275 <223> OTHER INFORMATION: is Thr, GABA, (D)- or (L)-1Nal, (D)- or (L)-2Nal, or (D)- or
(L
276      )-Phe
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Synthetic peptide
282 <400> SEQUENCE: 7
W--> 284 Xaa Xaa Xaa Lys Xaa Xaa Xaa
285      1      5
288 <210> SEQ ID NO: 8
289 <211> LENGTH: 9
290 <212> TYPE: PRT

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RAW SEQUENCE LISTING

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PATENT APPLICATION: US/09/734,583A

TIME: 14:52:42

Input Set : A:\87534-3000.txt

Output Set: N:\CRF4\11052004\I734583A.raw

*variable length not permitted
(see item 5 on Error Summary Sheet)*

291 <213> ORGANISM: Artificial Sequence
 293 <220> FEATURE:
 294 <221> NAME/KEY: MISC_FEATURE
 295 <222> LOCATION: (1)..(1)
 296 <223> OTHER INFORMATION: is absent or is a terminal group of four amino acids where
 some may be missing
 299 <220> FEATURE:
 300 <221> NAME/KEY: MISC_FEATURE
 301 <222> LOCATION: (2)..(2)
 302 <223> OTHER INFORMATION: is 1Nal, 2Nal, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or
 (D)
 303)- or (L)-Phe
 306 <220> FEATURE:
 307 <221> NAME/KEY: MISC_FEATURE
 308 <222> LOCATION: (3)..(4)
 309 <223> OTHER INFORMATION: may be absent, or are independently Gly, Tyr, 1Nal, 2Nal,
 Beta-As
 310 p (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe
 313 <220> FEATURE:
 314 <221> NAME/KEY: MISC_FEATURE
 315 <222> LOCATION: (5)..(5)
 316 <223> OTHER INFORMATION: (D)- or (L)-Trp
 319 <220> FEATURE:
 320 <221> NAME/KEY: MISC_FEATURE
 321 <222> LOCATION: (6)..(6)
 322 <223> OTHER INFORMATION: (D)- or (L)-Lys
 325 <220> FEATURE:
 326 <221> NAME/KEY: MISC_FEATURE
 327 <222> LOCATION: (7)..(7)
 328 <223> OTHER INFORMATION: is absent or is Gly, Abu, Cys, Thr, Val, (D)- or (L)-Ala, or
 (D)
 329 - or (L)-Phe
 332 <220> FEATURE:
 333 <221> NAME/KEY: MISC_FEATURE
 334 <222> LOCATION: (8)..(8)
 335 <223> OTHER INFORMATION: is Cys, (D)- or (L)-Ala, or (D)- or (L)-Phe
 338 <220> FEATURE:
 339 <221> NAME/KEY: MISC_FEATURE
 340 <222> LOCATION: (9)..(9)
 341 <223> OTHER INFORMATION: is absent or is Val, Thr, 1Nal or 2Nal
 344 <220> FEATURE:
 345 <223> OTHER INFORMATION: Synthetic peptide
 347 <400> SEQUENCE: 8
 W--> 349 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 350 1 5
 353 <210> SEQ ID NO: 9
 354 <211> LENGTH: 7
 355 <212> TYPE: PRT
 356 <213> ORGANISM: Artificial Sequence
 358 <220> FEATURE:
 359 <221> NAME/KEY: MISC_FEATURE
 360 <222> LOCATION: (1)..(1)
 361 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala; Residue 1 is

connected

RAW SEQUENCE LISTING ERROR SUMMARY
 PATENT APPLICATION: US/09/734,583A

DATE: 11/05/2004
 TIME: 14:52:43

FYI

Input Set : A:\87534-3000.txt
 Output Set: N:\CRF4\11052004\I734583A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 1,2,3,4,5,6,7,8
 Seq#:7; Xaa Pos. 1,2,3,4,5,6,7
 Seq#:8; Xaa Pos. 1,2,3,4,5,6,7,8,9
 Seq#:9; Xaa Pos. 1,2,3,4,5,6,7
 Seq#:10; Xaa Pos. 1,2,3,4,5,6,7

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:8; Line(s) 296

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/734,583A

DATE: 11/05/2004

TIME: 14:52:43

Input Set : A:\87534-3000.txt

Output Set: N:\CRF4\11052004\I734583A.raw

L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:132 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0

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